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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/616,849	07/14/2000	Julja Burchard	9301-044	6450

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EXAMINER	
FORMAN, BETTY J	
ART UNIT	PAPER NUMBER
1634	13

DATE MAILED: 09/25/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/616,849	BURCHARD, JULJA	
	Examiner	Art Unit	
	BJ Forman	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *15 July 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *27-30,33-40,42-54,57-68,71-75,84,85 and 90* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *27-30,33-40,42-54,57-68,71-75,84,85 and 90* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☒ Interview Summary (PTO-413) Paper No(s). *12* .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Continued Examination Under 37 CFR 1.114

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 15 July 2002 has been entered.

Amendments

2. This action is in response to papers filed 15 July 2002 in Paper No. 11 in which claims 27, 33-35, 42, 48-54, 57, 67 and 71 were amended, claims 1, 3-26, 55-56, 69-70 and 81-83 were canceled and claim 90 was added. All of the amendments have been thoroughly reviewed and entered. The previous rejections in the Office Action of Paper No. 8 dated 15 April 2002 are withdrawn in view of the amendments. All of the arguments have been thoroughly reviewed but are deemed moot in view of the amendments, withdrawn rejections and new grounds for rejection necessitated by amendments. New grounds for rejection are discussed.

Claims 27-30, 33-40, 42-54, 57-68, 71-75, 84-85 and 90 are under prosecution.

Claim Rejections - 35 USC § 112

3. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

4. Claims 48-50, 75 and 90 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

a. Claims 48-50 are each indefinite for the recitation "differs form the amount of the corresponding polynucleotide molecule" because "corresponding" is a non-specific relational term and therefore the relationship between the first and second sample polynucleotides is undefined. It is suggested that the claims be amended to define the relationship.

b. Claim 75 is indefinite for the recitation "wherein none of the plurality of different polynucleotide molecules" because it is unclear whether the recitation refers to the "two or more" in line 1 of Claim 75 or refers to the "plurality of different polynucleotide molecules" in the second sample of Claim 67. It is suggested that Claim 75 be amended to clarify.

c. Claim 90 is indefinite for the recitation "wherein said polynucleotide molecules comprising said target nucleotide sequences are the same" because it is unclear whether "said polynucleotides molecules" are one and the same molecule or whether "said polynucleotide molecules are the same sequence. It is suggested that Claim 90 be amended to clarify.

Claim Rejections - 35 USC § 102

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (e) the invention was described in-
> (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effect under this subsection of a national application published under section 122(b) only if the international

application designating the United States was published under Article 21(2)(a) of such treaty in the English language; or
(2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that a patent shall not be deemed filed in the United States for the purposes of this subsection based on the filing of an international application filed under the treaty defined in section 351(a).

6. Claims 27-30, 33-36, 44-47, 57-68, 71-75 and 90 are rejected under 35 U.S.C. 102(e) as being anticipated by Lockhart et al (U.S. Patent No. 6,344,316 B1, filed 25 June 1997).

Regarding Claim 27, Lockhart et al disclose a method for evaluating a binding property of a polynucleotide probe comprising a predetermined nucleotide sequence to a target nucleotide sequence, said method comprising: comparing the amount of hybridization of polynucleotide in a first sample to the probe with the amount of hybridization of polynucleotides in a second sample to the probe wherein the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence and said second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide comprises a sequences that is different from the sequences of other polynucleotides and wherein at least 75% of the polynucleotides in the first sample are polynucleotides comprising said target sequence thereby evaluating said binding property of said probe (Column 36, lines 24-47 and Example 1, Column 70, line 58-Column 73, line 46).

Regarding Claim 28, Lockhart et al disclose the method wherein the predetermined sequence of the probe is complementary to at least a hybridizable portion of the target sequence in the first sample (Column 36, lines 33-39).

Regarding Claim 29, Lockhart et al disclose the method wherein the target polynucleotide sequence in the first sequence is a sequence of a gene or gene transcript or of an mRNA, cDNA derived therefrom (Column 36, lines 24-47).

Regarding Claim 30, Lockhart et al disclose the method wherein the different polynucleotides in the second sample comprise sequences of a plurality of gene transcripts of a cell or organism (Column 36, lines 24-47).

Regarding Claims 33-35, Lockhart et al disclose the method wherein at least 90% (Claim 33); at least 95% (Claim 34); and at least 99% (Claim 35) of the polynucleotides in said first sample are polynucleotides comprising said target sequence i.e. "target nucleic acid alone" (Column 36, lines 33-35).

Regarding Claim 36, Lockhart et al disclose the method wherein each different polynucleotide in the second sample does not comprise the target sequence (Column 36, lines 33-37).

Regarding Claims 44-47, Lockhart et al disclose the method wherein the amount of polynucleotides in the first sample comprising the target sequence differs from the amount of polynucleotides in the second sample comprising the target sequence by at least a factor of four (Claim 44); by at least a factor of eight (Claim 45); by at least a factor of 20 (Claim 46); and by at least a factor of 100 (Claim 47) i.e. the second sample does not comprise the target sequence (Column 36, lines 33-37).

Regarding Claim 57, Lockhart et al disclose the method wherein said binding property is a specificity of the probe wherein said specificity is the amount of said polynucleotides comprising said target sequence that bind to said probe relative to the amount of polynucleotides not comprising said target sequence that bind to the probe under the same conditions i.e. little or no cross-hybridization (Column 36, lines 44-47).

Regarding Claim 58, Lockhart et al disclose the method wherein the specificity of the probe is determined from a ratio of the amount of hybridization of the polynucleotides comprising said target sequence in the first sample to the probe to the amount of hybridization of the plurality of different polynucleotides in the second sample to each probe i.e. little or no cross-hybridization (Column 36, lines 44-47).

Regarding Claim 59, Lockhart et al disclose the method wherein the polynucleotides in the first sample are detectably labeled (Column 24, lines 7-67).

Regarding Claim 60, Lockhart et al disclose the method wherein the polynucleotides in the second sample are detectably labeled (Column 24, lines 7-67).

Regarding Claim 61, Lockhart et al disclose the method wherein the polynucleotides are labeled with a fluorescent molecule (Column 24, lines 54-67).

Regarding Claim 62, Lockhart et al disclose the method wherein the polynucleotides in the first sample are labeled with a first label and the polynucleotides in the second sample are labeled with a second label the first label being distinguishable from the second (Column 24, lines 54-67).

Regarding Claim 63, Lockhart et al disclose the method wherein the first and second labels are fluorescent molecules (Column 24, lines 54-67).

Regarding Claim 64, Lockhart et al disclose the method wherein the probe is attached to a surface of a support (Column 36, lines 24-30).

Regarding Claim 65, Lockhart et al disclose the probe is one of a plurality of probes (Column 36, lines 24-30).

Regarding Claim 66, Lockhart et al disclose the method wherein the plurality of probes comprises polynucleotide probes in an array of probes said array having a support with at least one surface and different probes attached to said surface wherein each of said different probes attached is attached in a different location (Column 34, lines 24-30).

Regarding Claim 67, Lockhart et al disclose a method for evaluating a binding property of a plurality of polynucleotide probes to a target sequence wherein each probe comprises a predetermined nucleotide sequence, said method comprising comparing the amount of hybridization of polynucleotide in a first sample to each probe with the amount of hybridization of polynucleotides in a second sample to each probe wherein the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence and said second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide comprises a sequences that is different from the sequences of other

polynucleotides and wherein at least 75% of the polynucleotides in the first sample are polynucleotides comprising said target sequence thereby evaluating said binding property of said probe (Column 36, line 24-47).

Regarding Claim 68, Lockhart et al disclose the method wherein the predetermined sequence of each probe is complementary to at least a hybridizable portion of the target sequence in the first sample (Column 36, lines 33-39).

Regarding Claim 71, Lockhart et al disclose the method wherein said binding property is a specificity of each probe wherein said specificity is the amount of said polynucleotides comprising said target sequence that bind to said probe relative to the amount of polynucleotides not comprising said target sequence that bind to the probe under the same conditions i.e. little or no cross-hybridization (Column 36, lines 44-47).

Regarding Claim 72, Lockhart et al disclose the method wherein the specificity of each probe is determined from a ratio of the amount of hybridization of the polynucleotides comprising said target sequence in the first sample to each probe to the amount of hybridization of the plurality of different polynucleotides in the second sample to each probe i.e. little or no cross-hybridization (Column 36, lines 44-47).

Regarding Claim 73, Lockhart et al disclose the method wherein each probe is attached to a surface of a support (Column 36, lines 24-30).

Regarding Claim 74, Lockhart et al disclose the method wherein the plurality of probes comprises polynucleotide probes in an array of probes said array having a support with at least one surface and different probes attached to said surface wherein each of said different probes attached is attached in a different location (Column 34, lines 24-30).

Regarding Claim 75, Lockhart et al disclose the method wherein the first sample comprises two or more different polynucleotide molecules (i.e. "probes of the high density array are then hybridized with their target") wherein none of the plurality of different polynucleotide

molecules hybridizes or cross-hybridizes to a probe that also hybridizes or cross-hybridizes to another of the plurality of different polynucleotide molecules (Column 36, lines 24-47).

Regarding Claim 90. Lockhart et al disclose the method wherein the polynucleotide molecules comprising the target sequence are the same (Column 36, lines 33-34).

Claim Rejections - 35 USC § 103

7. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

8. Claims 37-40, 42, 43, 48-54, 84, 85 and 90 are rejected under 35 U.S.C. 103(a) as being unpatentable over Lockhart et al (U.S. Patent No. 6,344,316 B1, filed 25 June 1997) in view of Brown et al (U.S. Patent No. 5,807,522, issued 15 September 1998).

Regarding Claim 37, Lockhart et al teach a method for evaluating a binding property of a polynucleotide probe comprising a predetermined nucleotide sequence to a target nucleotide sequence, said method comprising: comparing the amount of hybridization of polynucleotide in a first sample to the probe with the amount of hybridization of polynucleotides in a second sample to the probe wherein the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence and said second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide comprises a sequences that is different from the sequences of other polynucleotides and wherein at least 75% of the

polynucleotides in the first sample are polynucleotides comprising said target sequence thereby evaluating said binding property of said probe wherein each different polynucleotide in the second sample does not comprise the target sequence wherein the target sequence is a gene sequence and wherein the probes comprise perfect match and mismatch probes (Column 36, lines 24-47 and Example 1, Column 70, line 58-Column 73, line 46) but they do not specifically teach the second sample comprises a sample from a deletion mutation. Brown et al. teach a similar method for evaluating binding of a plurality of polynucleotide probes to a target polynucleotide wherein each probe has a particular nucleotide sequence, said method comprising comparing the amount of hybridization in a first sample to the amount of hybridization in a second sample and wherein the first sample comprises a plurality of the same target polynucleotides (i.e. amplified copies of fragments from the large chromosomes) and the second sample comprises a plurality of different polynucleotide molecules wherein the different polynucleotide molecules have a different nucleotide sequence (i.e. the second sample comprises amplified copies of fragments from the small chromosomes) (Example 1, Column 16, line 39-56) wherein the target polynucleotide in the first sample corresponds to a gene or gene transcript i.e. the target is from a chromosome which contains genes and therefore the target "corresponds" to a gene (Column 16, lines 39-45) and they teach an embodiment of their method wherein the second sample comprises a sample from a deletion mutant wherein the deletion mutant does not express the gene (Column 15, lines 5-18). It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to modify the polynucleotides in the second sample of Lockhart et al with the deletion mutation of Brown et al. to thereby analyze and evaluate mutation-specific probes for the obvious benefits of providing accurate means of mutation detection and diagnosis.

Regarding Claim 38, Brown et al. teach the method wherein the polynucleotides in the second sample comprises polynucleotides having the same sequence as polynucleotides in the first sample and a plurality of different polynucleotides i.e. the different polynucleotides

produce a green signal and the polynucleotides having the same sequence produce an orange signal (Column 17, lines 9-17). It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to modify the polynucleotides in the second sample of Lockhart et al by including the target sequence along with the plurality of different sequences as taught by Brown et al. to thereby analyze and evaluate cross-hybridization of the probes for the obvious benefits of providing accurate means of mutation detection and diagnosis.

Regarding Claim 39, Lockhart et al teach the method wherein the target sequence comprises the sequence of a gene transcript and the second sample comprises a sample from a wild-type strain (Column 36,lines 24-47)

Regarding Claim 40, Lockhart et al teach the method wherein the first sample comprises target sequence and the second sample lack polynucleotides comprising the target sequence (Column 36, lines 24-47) but they do not teach the first sample comprises molecules that do not comprise the target sequence. Brown et al. teach the similar method wherein the first sample comprises polynucleotide molecules having a sequence different from the target polynucleotide (i.e. the sample has more than one different polynucleotides of different sequence) and the second sample lacks the different polynucleotides i.e. the red fluorescent signal identifies polynucleotides in the first sample lacking in the second sample (Column 17, lines 9-17). It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to modify the first sample of Lockhart et al by adding molecules not comprising the target sequence as taught by Brown et al and to analyze cross-hybridization between target-specific probes to thereby select non-cross-hybridizing probes for the obvious benefits of providing means for accurate sequence hybridization and analysis.

Regarding Claim 42, Lockhart et al teach the method wherein the target sequence is a gene transcript and the first sample comprises a sample from a wild-type cell which expressed the gene transcripts (Column 36, lines 24-47) but they do not teach the second sample comprising a sample from a deletion which does not express the gene transcript. Brown et al.

teach the similar method wherein the second sample comprises a sample from a deletion mutant wherein the deletion mutant does not express the gene (Column 15, lines 5-18). It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to modify the polynucleotides in the second sample of Lockhart et al with the deletion mutation of Brown et al. to thereby analyze and evaluate mutation-specific probes for the obvious benefits of providing accurate means of mutation detection and diagnosis.

Regarding Claim 43, Lockhart et al teach the method wherein the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence and said second sample comprises a plurality of different polynucleotide molecules wherein the amount of polynucleotides in the first sample comprising the target sequence differs from the amount of polynucleotides in the second sample comprising the target sequence by at least a factor of four i.e. the second sample does not comprise the target sequence (Column 36, lines 24-47) but they do not teach the first sample comprises molecules that do not contain the target sequence and the second sample comprises the molecules comprising the target sequence. Brown et al. teach the similar method wherein the first sample comprises polynucleotide molecules having a sequence different from the target polynucleotide (i.e. the sample has more than one different polynucleotide of different sequence) and the second sample comprises polynucleotides having the same sequence as the target and a plurality of different polynucleotides i.e. the green fluorescent signal identifies polynucleotides in the first sample lacking in the second sample, the red fluorescent signal identifies polynucleotides different from the first sample and yellow fluorescent signal identifies polynucleotides common between the samples (Column 18, lines 5-17).). It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to modify the first sample of Lockhart et al by adding molecules not comprising the target sequence as taught by Brown et al and to analyze cross-hybridization between target-specific probes to thereby select non-

cross-hybridizing probes for the obvious benefits of providing means for accurate sequence hybridization and analysis.

Regarding Claim 48-54, Lockhart et al teach the method wherein the first sample does not contain polynucleotides comprising the target sequence (Column 36, lines 24-47) However, Brown et al. teach the similar method wherein the amount of the polynucleotides in the first and second sample differ by no more than a factor of 100 (Claim 48); differ by no more than a factor of 10 (Claim 49); differ by no more than 50% (Claim 50); differ by no more than a factor of two (Claim 51); and the abundances differ no more than 50% (Claim 52); by nor more than 10% (Claim 53); and differ by no more than 1% (Claim 54); i.e. the amount and abundance are the same (Column 17, lines 65-67). It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to apply the equal amount and abundance of polynucleotides as taught by Brown et al to the probe analysis samples of Lockhart et al to thereby control sample quantities based on experimental design and thereby evaluate probe binding under controlled conditions for the obvious benefits of accurately evaluating probe binding during desired experimental conditions.

Regarding Claim 84, Lockhart et al teach the method wherein the polynucleotides in the first sample are labeled with a first label and the polynucleotides in the second sample are labeled with a second label the first label being distinguishable from the second (Column 24, lines 54-67) but they do not teach the step of comparing comprises concurrently contacting the probe with the first and second sample. However, Brown et al. teach the similar method wherein polynucleotides in the first sample are labeled with a first label and polynucleotides in the second sample are labeled with a second label distinguishable from the first label and further comprising concurrently contacting the probe with the first and second sample under conditions conductive to hybridization and detecting binding that occurs between the probe and polynucleotides in the first and second sample (Column 16, line 57-Column 17, line 8). It would have been obvious to one of ordinary skill in the art at the time the claimed invention

was made to modify the sequential hybridization of Lockhart et al with the concurrent hybridization of Brown et al and to hybridize the first and second samples to the probes concurrently thereby eliminating Lockhart's second hybridization step for the obvious benefits of simplification and economy of time.

Regarding Claim 85, Lockhart et al teach the method wherein the second sample lacks polynucleotides of the first sample (Column 36, lines 24-47).

Regarding Claim 90. Lockhart et al teach the method wherein the polynucleotide molecules comprising the target sequence are the same (Column 36, lines 33-34).

Conclusion

9. No claim is allowed.

10. Any inquiry concerning this communication or earlier communications from the examiner should be directed to BJ Forman whose telephone number is (703) 306-5878. The examiner can normally be reached on 6:30 TO 4:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones can be reached on (703) 308-1152. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 308-4242 for regular communications and (703) 308-8724 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

BJ Forman, Ph.D.
Patent Examiner
Art Unit: 1634
September 18, 2002

Interview Summary	Application No.	Applicant(s)	
	09/616,849	BURCHARD, JULJA	
	Examiner	Art Unit	
	BJ Forman	1634	

All participants (applicant, applicant's representative, PTO personnel):

(1) *BJ Forman*. (3)*Doug Bradley*.

(2) *Adrian Antler*. (4)_____.

Date of Interview: *02 July 2002* .

Type: a)☒ Telephonic b)☐ Video Conference
c)☐ Personal [copy given to: 1)☐ applicant 2)☐ applicant's representative]

Exhibit shown or demonstration conducted: d)☐ Yes e)☐ No.
If Yes, brief description: _____ .

Claim(s) discussed: *all* .

Identification of prior art discussed: _____ .

Agreement with respect to the claims f)☐ was reached. g)☒ was not reached. h)☐ N/A.

Substance of Interview including description of the general nature of what was agreed to if an agreement was reached, or any other comments: *See Continuation Sheet* .

(A fuller description, if necessary, and a copy of the amendments which the examiner agreed would render the claims allowable, if available, must be attached. Also, where no copy of the amendments that would render the claims allowable is available, a summary thereof must be attached.)

i)☐ It is not necessary for applicant to provide a separate record of the substance of the interview(if box is checked).

Unless the paragraph above has been checked, THE FORMAL WRITTEN REPLY TO THE LAST OFFICE ACTION MUST INCLUDE THE SUBSTANCE OF THE INTERVIEW. (See MPEP Section 713.04). If a reply to the last Office action has already been filed, APPLICANT IS GIVEN ONE MONTH FROM THIS INTERVIEW DATE TO FILE A STATEMENT OF THE SUBSTANCE OF THE INTERVIEW. See Summary of Record of Interview requirements on reverse side or on attached sheet.

Examiner Note: You must sign this form unless it is an Attachment to a signed Office action.

Examiner's signature, if required

Continuation of Substance of Interview including description of the general nature of what was agreed to if an agreement was reached, or any other comments: Applicant FAX'd proposed amendments to the claims which were discussed during the interview. Additionally, Ms. Antler stated that additional claims would be cancelled and/or amended in the formal response. The examiner informed Applicants that the proposed amendments would overcome the rejections of the Final Office Action, and that the amendments redefine the invention. The examiner stated that if filed as an After Final Amendment, it was most likely that they would not bee entered because the amendments which redefine the invention would require further search and consideration. The examiner also requested that Applicant, in their response, point to passages within the specification that provide support for the amendments. Ms. Antler asked if it would be best to file an RCE. The examiner agreed that given the redefinition of the invention, filing an RCE would be most appropriate at this point. .